



2590  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/983,025A

DATE: 01/29/2003 *fb*

TIME: 13:54:04

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\01292003\I983025A.raw

3 <110> APPLICANT: OXVIG, Claus  
 4 OVERGAARD, Michael T.  
 6 <120> TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)  
 8 <130> FILE REFERENCE: OXVIG=1A  
 10 <140> CURRENT APPLICATION NUMBER: US 09/983,025A  
 11 <141> CURRENT FILING DATE: 2001-10-22  
 13 <150> PRIOR APPLICATION NUMBER: US 60/241,840  
 14 <151> PRIOR FILING DATE: 2000-10-20  
 16 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01571  
 17 <151> PRIOR FILING DATE: 2000-10-20  
 19 <160> NUMBER OF SEQ ID NOS: 26  
 21 <170> SOFTWARE: PatentIn version 3.2  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 8527  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (1)..(5373)  
 32 <223> OTHER INFORMATION: prepro-PAPP-A2 coding sequence  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: sig\_peptide  
 36 <222> LOCATION: (1)..(66)  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: misc\_feature  
 40 <222> LOCATION: (1)..(66)  
 41 <223> OTHER INFORMATION: prepro part of PAPP-A2  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: misc\_feature  
 45 <222> LOCATION: (67)..(699)  
 46 <223> OTHER INFORMATION: pro part of PAPP-A2  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: mat\_peptide  
 50 <222> LOCATION: (700)..()  
 52 <220> FEATURE:  
 53 <221> NAME/KEY: 3'UTR  
 54 <222> LOCATION: (5377)..(8527)  
 56 <400> SEQUENCE: 1  
 57 atg atg tgc tta aag atc cta aga ata agc ctg gcg att ttg gct 45  
 58 Met Met Cys Leu Lys Ile Leu Arg Ile Ser Leu Ala Ile Leu Ala  
 59 -230 -225 -220  
 61 ggg tgg gca ctc tgt tct gcc aac tct gag ctg ggc tgg aca cgc 90  
 62 Gly Trp Ala Leu Cys Ser Ala Asn Ser Glu Leu Gly Trp Thr Arg

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63	-215	-210	-205	
65	aag aaa tcc ttg	gtt gag agg gaa cac	ctg aat cag gtg ctg ttg	135
66	Lys Lys Ser Leu	Val Glu Arg Glu His	Leu Asn Gln Val Leu Leu	
67	-200	-195	-190	
69	gaa gga gaa cgt	tgt tgg ctg ggg gcc	aag gtt cga aga ccc aga	180
70	Glu Gly Glu Arg	Cys Trp Leu Gly Ala	Lys Val Arg Arg Pro Arg	
71	-185	-180	-175	
73	gct tct cca cag	cat cac ctc ttt gga	gtc tac ccc agc agg gct	225
74	Ala Ser Pro Gln	His His Leu Phe Gly	Val Tyr Pro Ser Arg Ala	
75	-170	-165	-160	
77	ggg aac tac cta	agg ccc tac ccc gtg	ggg gag caa gaa atc cat	270
78	Gly Asn Tyr Leu	Arg Pro Tyr Pro Val	Gly Glu Gln Glu Ile His	
79	-155	-150	-145	
81	cat aca gga cgc	agc aaa cca gac act	gaa gga aat gct gtg agc	315
82	His Thr Gly Arg	Ser Lys Pro Asp Thr	Glu Gly Asn Ala Val Ser	
83	-140	-135	-130	
85	ctt gtt ccc cca	gac ctg act gaa aat	cca gca gga ctg agg ggt	360
86	Leu Val Pro Pro	Asp Leu Thr Glu Asn	Pro Ala Gly Leu Arg Gly	
87	-125	-120	-115	
89	gca gtt gaa gag	ccg gct gcc cca tgg	gta ggg gat agt cct att	405
90	Ala Val Glu Glu	Pro Ala Ala Pro Trp	Val Gly Asp Ser Pro Ile	
91	-110	-105	-100	
93	ggg caa tct gag	ctg ctg gga gat gat	gac gct tat ctc ggc aat caa	453
94	Gly Gln Ser Glu	Leu Leu Gly Asp Asp	Asp Ala Tyr Leu Gly Asn Gln	
95	-95	-90	-85	
97	aga tcc aag gag	tct cta ggt gag gcc	ggg att cag aaa ggc tca gcc	501
98	Arg Ser Lys Glu	Ser Leu Gly Glu Ala	Gly Ile Gln Lys Gly Ser Ala	
99	-80	-75	-70	
101	atg gct gcc act	act acc acc gcc att	ttc aca acc ctg aac gaa ccc	549
102	Met Ala Ala Thr	Thr Thr Thr Thr Ala	Ile Phe Thr Thr Leu Asn Glu Pro	
103	-65	-60	-55	
105	aaa cca gag acc	caa agg agg ggc tgg	gcc aag tcc agg cag cgt cgc	597
106	Lys Pro Glu Thr	Gln Arg Arg Gly Trp	Ala Lys Ser Arg Gln Arg Arg	
107	-50	-45	-40	-35
109	caa gtg tgg aag	agg cgg gcg gaa gat	ggg cag gga gac tcc ggt atc	645
110	Gln Val Trp Lys	Arg Arg Ala Glu Asp	Gly Gln Gly Asp Ser Gly Ile	
111	-30	-25	-20	
113	tct tca cat ttc	caa cct tgg ccc aag	cat tcc ctt aaa cac agg gtc	693
114	Ser Ser His Phe	Gln Pro Trp Pro Lys	His Ser Leu Lys His Arg Val	
115	-15	-10	-5	
117	aaa aag agt cca	ccg gag gaa agc aac	caa aat ggt gga gag ggc tcc	741
118	Lys Lys Ser Pro	Pro Glu Glu Ser Asn	Gln Asn Gly Gly Glu Gly Ser	
119	-1 1	5	10	
121	tac cga gaa gca	gag acc ttt aac tcc	caa gta gga ctg ccc atc tta	789
122	Tyr Arg Glu Ala	Glu Thr Phe Asn Ser	Gln Val Gly Leu Pro Ile Leu	
123	15	20	25	30
125	tac ttc tct ggg	agg cgg gag cgg ctg	ctg ctg cgt cca gaa gtg ctg	837
126	Tyr Phe Ser Gly	Arg Arg Glu Arg Leu	Leu Leu Arg Pro Glu Val Leu	
127	35	40	45	

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129	gct	gag	att	ccc	cgg	gag	gcg	ttc	aca	gtg	gaa	gcc	tgg	gtt	aaa	ccg	885
130	Ala	Glu	Ile	Pro	Arg	Glu	Ala	Phe	Thr	Val	Glu	Ala	Trp	Val	Lys	Pro	
131				50					55					60			
133	gag	gga	gga	cag	aac	aac	cca	gcc	atc	atc	gca	ggt	gtg	ttt	gat	aac	933
134	Glu	Gly	Gly	Gln	Asn	Asn	Pro	Ala	Ile	Ile	Ala	Gly	Val	Phe	Asp	Asn	
135				65				70					75				
137	tgc	tcc	cac	act	gtc	agt	gac	aaa	ggc	tgg	gcc	ctg	ggg	atc	cgc	tca	981
138	Cys	Ser	His	Thr	Val	Ser	Asp	Lys	Gly	Trp	Ala	Leu	Gly	Ile	Arg	Ser	
139		80					85					90					
141	ggg	aag	gac	aag	gga	aag	cgg	gat	gct	cgc	ttc	ttc	ttc	tcc	ctc	tgc	1029
142	Gly	Lys	Asp	Lys	Gly	Lys	Arg	Asp	Ala	Arg	Phe	Phe	Phe	Ser	Leu	Cys	
143	95						100				105					110	
145	acc	gac	cgc	gtg	aag	aaa	gcc	acc	atc	ttg	att	agc	cac	agt	cgc	tac	1077
146	Thr	Asp	Arg	Val	Lys	Lys	Ala	Thr	Ile	Leu	Ile	Ser	His	Ser	Arg	Tyr	
147					115					120					125		
149	caa	cca	ggc	aca	tgg	acc	cat	gtg	gca	gcc	act	tac	gat	gga	cgg	cac	1125
150	Gln	Pro	Gly	Thr	Trp	Thr	His	Val	Ala	Ala	Thr	Tyr	Asp	Gly	Arg	His	
151				130					135					140			
153	atg	gcc	ctg	tat	gtg	gat	ggc	act	cag	gtg	gct	agc	agt	cta	gac	cag	1173
154	Met	Ala	Leu	Tyr	Val	Asp	Gly	Thr	Gln	Val	Ala	Ser	Ser	Leu	Asp	Gln	
155				145				150					155				
157	tct	ggt	ccc	ctg	aac	agc	ccc	ttc	atg	gca	tct	tgc	cgc	tct	ttg	ctc	1221
158	Ser	Gly	Pro	Leu	Asn	Ser	Pro	Phe	Met	Ala	Ser	Cys	Arg	Ser	Leu	Leu	
159		160					165					170					
161	ctg	ggg	gga	gac	agc	tct	gag	gat	ggg	cac	tat	ttc	cgt	gga	cac	ctg	1269
162	Leu	Gly	Gly	Asp	Ser	Ser	Glu	Asp	Gly	His	Tyr	Phe	Arg	Gly	His	Leu	
163	175						180				185					190	
165	ggc	aca	ctg	gtt	ttc	tgg	tcg	acc	gcc	ctg	cca	caa	agc	cat	ttt	cag	1317
166	Gly	Thr	Leu	Val	Phe	Trp	Ser	Thr	Ala	Leu	Pro	Gln	Ser	His	Phe	Gln	
167					195					200					205		
169	cac	agt	tct	cag	cat	tca	agt	ggg	gag	gag	gaa	gcg	act	gac	ttg	gtc	1365
170	His	Ser	Ser	Gln	His	Ser	Ser	Gly	Glu	Glu	Glu	Ala	Thr	Asp	Leu	Val	
171				210					215					220			
173	ctg	aca	gcg	agc	ttt	gag	cct	gtg	aac	aca	gag	tgg	gtt	ccc	ttt	aga	1413
174	Leu	Thr	Ala	Ser	Phe	Glu	Pro	Val	Asn	Thr	Glu	Trp	Val	Pro	Phe	Arg	
175				225					230					235			
177	gat	gag	aag	tac	cca	cga	ctt	gag	gtt	ctc	cag	ggc	ttt	gag	cca	gag	1461
178	Asp	Glu	Lys	Tyr	Pro	Arg	Leu	Glu	Val	Leu	Gln	Gly	Phe	Glu	Pro	Glu	
179		240					245					250					
181	cct	gag	att	ctg	tcg	cct	ttg	cag	ccc	cca	ctc	tgt	ggg	caa	aca	gtc	1509
182	Pro	Glu	Ile	Leu	Ser	Pro	Leu	Gln	Pro	Pro	Leu	Cys	Gly	Gln	Thr	Val	
183	255						260					265				270	
185	tgt	gac	aat	gtg	gaa	ttg	atc	tcc	cag	tac	aat	gga	tac	tgg	ccc	ctt	1557
186	Cys	Asp	Asn	Val	Glu	Leu	Ile	Ser	Gln	Tyr	Asn	Gly	Tyr	Trp	Pro	Leu	
187					275					280					285		
189	cgg	gga	gag	aag	gtg	ata	cgc	tac	cag	gtg	gtg	aac	atc	tgt	gat	gat	1605
190	Arg	Gly	Glu	Lys	Val	Ile	Arg	Tyr	Gln	Val	Val	Asn	Ile	Cys	Asp	Asp	
191				290					295					300			
193	gag	ggc	cta	aac	ccc	att	gtg	agt	gag	gag	cag	att	cgt	ctg	cag	cac	1653

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194	Glu	Gly	Leu	Asn	Pro	Ile	Val	Ser	Glu	Glu	Gln	Ile	Arg	Leu	Gln	His	
195			305					310					315				
197	gag	gca	ctg	aat	gag	gcc	ttc	agc	cgc	tac	aac	atc	agc	tgg	cag	ctg	1701
198	Glu	Ala	Leu	Asn	Glu	Ala	Phe	Ser	Arg	Tyr	Asn	Ile	Ser	Trp	Gln	Leu	
199		320					325					330					
201	agc	gtc	cac	cag	gtc	cac	aat	tcc	acc	ctg	cga	cac	cgg	gtt	gtg	ctt	1749
202	Ser	Val	His	Gln	Val	His	Asn	Ser	Thr	Leu	Arg	His	Arg	Val	Val	Leu	
203	335					340					345					350	
205	gtg	aac	tgt	gag	ccc	agc	aag	att	ggc	aat	gac	cat	tgt	gac	ccc	gag	1797
206	Val	Asn	Cys	Glu	Pro	Ser	Lys	Ile	Gly	Asn	Asp	His	Cys	Asp	Pro	Glu	
207					355					360					365		
209	tgt	gag	cac	cca	ctc	aca	ggc	tat	gat	ggg	ggt	gac	tgc	cgc	ctg	cag	1845
210	Cys	Glu	His	Pro	Leu	Thr	Gly	Tyr	Asp	Gly	Gly	Asp	Cys	Arg	Leu	Gln	
211				370					375					380			
213	ggc	cgc	tgc	tac	tcc	tgg	aac	cgc	agg	gat	ggg	ctc	tgt	cac	gtg	gag	1893
214	Gly	Arg	Cys	Tyr	Ser	Trp	Asn	Arg	Arg	Asp	Gly	Leu	Cys	His	Val	Glu	
215			385					390					395				
217	tgt	aac	aac	atg	ctg	aac	gac	ttt	gac	gac	gga	gac	tgc	tgc	gac	ccc	1941
218	Cys	Asn	Asn	Met	Leu	Asn	Asp	Phe	Asp	Asp	Gly	Asp	Cys	Cys	Asp	Pro	
219		400					405					410					
221	cag	gtg	gct	gat	gtg	cgc	aag	acc	tgc	ttt	gac	cct	gac	tca	ccc	aag	1989
222	Gln	Val	Ala	Asp	Val	Arg	Lys	Thr	Cys	Phe	Asp	Pro	Asp	Ser	Pro	Lys	
223	415					420				425						430	
225	agg	gca	tac	atg	agt	gtg	aag	gag	ctg	aag	gag	gcc	ctg	cag	ctg	aac	2037
226	Arg	Ala	Tyr	Met	Ser	Val	Lys	Glu	Leu	Lys	Glu	Ala	Leu	Gln	Leu	Asn	
227					435					440					445		
229	agt	act	cac	ttc	ctc	aac	atc	tac	ttt	gcc	agc	tca	gtg	cgg	gaa	gac	2085
230	Ser	Thr	His	Phe	Leu	Asn	Ile	Tyr	Phe	Ala	Ser	Ser	Val	Arg	Glu	Asp	
231				450					455					460			
233	ctt	gca	ggt	gct	gcc	acc	tgg	cct	tgg	gac	aag	gac	gct	gtc	act	cac	2133
234	Leu	Ala	Gly	Ala	Ala	Thr	Trp	Pro	Trp	Asp	Lys	Asp	Ala	Val	Thr	His	
235			465					470					475				
237	ctg	ggt	ggc	att	gtc	ctc	agc	cca	gca	tat	tat	ggg	atg	cct	ggc	cac	2181
238	Leu	Gly	Gly	Ile	Val	Leu	Ser	Pro	Ala	Tyr	Tyr	Gly	Met	Pro	Gly	His	
239		480					485					490					
241	acc	gac	acc	atg	atc	cat	gaa	gtg	gga	cat	gtt	ctg	gga	ctc	tac	cat	2229
242	Thr	Asp	Thr	Met	Ile	His	Glu	Val	Gly	His	Val	Leu	Gly	Leu	Tyr	His	
243	495					500					505					510	
245	gtc	ttt	aaa	gga	gtc	agt	gaa	aga	gaa	tcc	tgc	aat	gac	ccc	tgc	aag	2277
246	Val	Phe	Lys	Gly	Val	Ser	Glu	Arg	Glu	Ser	Cys	Asn	Asp	Pro	Cys	Lys	
247					515					520					525		
249	gag	aca	gtg	cca	tcc	atg	gaa	acg	gga	gac	ctc	tgt	gcc	gac	acc	gcc	2325
250	Glu	Thr	Val	Pro	Ser	Met	Glu	Thr	Gly	Asp	Leu	Cys	Ala	Asp	Thr	Ala	
251				530					535					540			
253	ccc	act	ccc	aag	agt	gag	ctg	tgc	cgg	gaa	cca	gag	ccc	act	agt	gac	2373
254	Pro	Thr	Pro	Lys	Ser	Glu	Leu	Cys	Arg	Glu	Pro	Glu	Pro	Thr	Ser	Asp	
255			545					550					555				
257	acc	tgt	ggc	ttc	act	cgc	ttc	cca	ggg	gct	ccg	ttc	acc	aac	tac	atg	2421
258	Thr	Cys	Gly	Phe	Thr	Arg	Phe	Pro	Gly	Ala	Pro	Phe	Thr	Asn	Tyr	Met	

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259	560	565	570	
261	agc tac acg gat gat aac tgc act gac aac ttc act cct aac caa gtg	2469		
262	Ser Tyr Thr Asp Asp Asn Cys Thr Asp Asn Phe Thr Pro Asn Gln Val			
263	575 580 585 590			
265	gcc cga atg cat tgc tat ttg gac cta gtc tat cag cag tgg act gaa	2517		
266	Ala Arg Met His Cys Tyr Leu Asp Leu Val Tyr Gln Gln Trp Thr Glu			
267	595 600 605			
269	agc aga aag ccc acc ccc atc ccc att cca cct atg gtc atc gga cag	2565		
270	Ser Arg Lys Pro Thr Pro Ile Pro Ile Pro Pro Met Val Ile Gly Gln			
271	610 615 620			
273	acc aac aag tcc ctc act atc cac tgg ctg cct cct att agt gga gtt	2613		
274	Thr Asn Lys Ser Leu Thr Ile His Trp Leu Pro Pro Ile Ser Gly Val			
275	625 630 635			
277	gta tat gac agg gcc tca ggc agc ttg tgt ggc gct tgc act gaa gat	2661		
278	Val Tyr Asp Arg Ala Ser Gly Ser Leu Cys Gly Ala Cys Thr Glu Asp			
279	640 645 650			
281	ggg acc ttt cgt cag tat gtg cac aca gct tcc tcc cgg cgg gtg tgt	2709		
282	Gly Thr Phe Arg Gln Tyr Val His Thr Ala Ser Ser Arg Arg Val Cys			
283	655 660 665 670			
285	gac tcc tca ggt tat tgg acc cca gag gag gct gtg ggg cct cct gat	2757		
286	Asp Ser Ser Gly Tyr Trp Thr Pro Glu Glu Ala Val Gly Pro Pro Asp			
287	675 680 685			
289	gtg gat cag ccc tgc gag cca agc tta cag gcc tgg agc cct gag gtc	2805		
290	Val Asp Gln Pro Cys Glu Pro Ser Leu Gln Ala Trp Ser Pro Glu Val			
291	690 695 700			
293	cac ctg tac cac atg aac atg acg gtc ccc tgc ccc aca gaa ggc tgt	2853		
294	His Leu Tyr His Met Asn Met Thr Val Pro Cys Pro Thr Glu Gly Cys			
295	705 710 715			
297	agc ttg gag ctg ctc ttc caa cac ccg gtc caa gcc gac acc ctc acc	2901		
298	Ser Leu Glu Leu Leu Phe Gln His Pro Val Gln Ala Asp Thr Leu Thr			
299	720 725 730			
301	ctg tgg gtc act tcc ttc ttc atg gag tcc tcg cag gtc ctc ttt gac	2949		
302	Leu Trp Val Thr Ser Phe Phe Met Glu Ser Ser Gln Val Leu Phe Asp			
303	735 740 745 750			
305	aca gag atc ttg ctg gaa aac aag gag tca gtg cac ctg ggc ccc tta	2997		
306	Thr Glu Ile Leu Leu Glu Asn Lys Glu Ser Val His Leu Gly Pro Leu			
307	755 760 765			
309	gac act ttc tgt gac atc cca ctc acc atc aaa ctg cac gtg gat ggg	3045		
310	Asp Thr Phe Cys Asp Ile Pro Leu Thr Ile Lys Leu His Val Asp Gly			
311	770 775 780			
313	aag gtg tcg ggg gtg aaa gtc tac acc ttt gat gag agg ata gag att	3093		
314	Lys Val Ser Gly Val Lys Val Tyr Thr Phe Asp Glu Arg Ile Glu Ile			
315	785 790 795			
317	gat gca gca ctc ctg act tct cag ccc cac agt ccc ttg tgc tct ggc	3141		
318	Asp Ala Ala Leu Leu Thr Ser Gln Pro His Ser Pro Leu Cys Ser Gly			
319	800 805 810			
321	tgc agg cct gtg agg tac cag gtt ctc cgc gat ccc cca ttt gcc agt	3189		
322	Cys Arg Pro Val Arg Tyr Gln Val Leu Arg Asp Pro Pro Phe Ala Ser			
323	815 820 825 830			

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3,4,6,7,9,10  
Seq#:24; Xaa Pos. 3  
Seq#:26; Xaa Pos. 3,4,6,7,9,10

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:26

## VERIFICATION SUMMARY

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L:1132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:1402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0